

Figure 1

1	MRPSIHRTAI AAVLATAFVA GTALAQKRDN VLFQAATDEQ PAVIKTLEKL	50
51	VNIETGTGDA EGIAAAGNFL EAEELKNLGFT VTRSKSAGLV VGDNIVGKIK	100
101	GRGGKNLLLM SHMDTVYLKG ILAKAPFRVE GDKAYGPGIA DDKGGNAVIL	150
151	HTLKLLKEYG VRDYGTTITVL FNTDEEKGSF GSRDLIQEEA KLADYVLSFE	200
201	PTSAGDEKLS LGTSGIAYVQ VNITGKASHA GAAPELGVNA LVEASDLVLR	250
251	TMNIDDKAKN LRFNWTIAKA GNVSNIIPAS ATLNADVRYA RNEDFDAAMK	300
301	TLEERAQQKK LPEADVKVIV TRGRPAFNAG EGGKKLVDKA VAYYKEAGGT	350
351	LGVEERTGGG TDAAYAALSG KPVIESLGLP GFGYHSDKAE YVDISAIIPRR	400
401	LYMAARLIMD LGAGK	415

Figure 2